

Compound	R	R <sup>1</sup>	Sequence, 5' to 3'	X <sup>a</sup>	Retention time, min <sup>b</sup>	
					Gradient 1	Gradient 2
8	TMT	H	T <sub>12</sub> <SEQ. ID. NO. 1>	O	32.8	-
9	TMT	H	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	27.7	23.8
10	TMT	Pyr	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	-	30.2, 30.7
11	TMT	Pyr	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	O	-	29.1
12	TMT	Flu	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	33.4, 34.2	-
13	TMT	Flu	<i>AGCT<sub>2</sub>C T<sub>3</sub>GCACA TGTA<sub>3</sub></i> <sup>c</sup>	S	35.9, 36.3	-
			<SEQ. ID. NO. 3>			
14	TMT	Flu	T <sub>12</sub> <SEQ. ID. NO. 1>	O	32.9	-
15	TMT	C <sub>2</sub> H <sub>5</sub>	T <sub>12</sub> <SEQ. ID. NO. 1>	O	33.0	-
16	H	H	T <sub>12</sub> <SEQ. ID. NO. 1>	O	18.0	-
17	H	H	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	19.6	16.4
18	H	Pyr	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	-	25.0
19	H	Pyr	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	O	-	24.5
20	H	Flu	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	23.4	-
21	H	Flu	<i>AGCT<sub>2</sub>C T<sub>3</sub>GCACA TGTA<sub>3</sub></i> <sup>c</sup>	S	28.5	-
			<SEQ. ID. NO. 3>			
22	H	Flu	T <sub>12</sub> <SEQ. ID. NO. 1>	O	22.7	-
23	H	C <sub>2</sub> H <sub>5</sub>	T <sub>12</sub> <SEQ. ID. NO. 1>	O	21.5	-
24	-	H	T <sub>12</sub> <SEQ. ID. NO. 1>	O	16.2	-
25	-	H	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	18.0	15.2
26	-	Pyr	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	22.6	17.1
27	-	Pyr	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	O	22.0	16.7
28	-	Flu	ATGCAT <sub>2</sub> CTGC <sub>5</sub> A <sub>2</sub> G <sub>2</sub> A <SEQ. ID. NO. 2>	S	19.1	14.5
29	-	Flu	<i>AGCT<sub>2</sub>C T<sub>3</sub>GCACA TGTA<sub>3</sub></i> <sup>c</sup>	S	21.7	-
			<SEQ. ID. NO. 3>			
30	-	Flu	T <sub>12</sub> <SEQ. ID. NO. 1>	O	18.1	-
31	-	C <sub>2</sub> H <sub>5</sub>	T <sub>12</sub> <SEQ. ID. NO. 1>	O	17.9	-

<sup>a</sup> All oligonucleotides contained uniform, either phosphate (X=O) or phosphorothioate (X=S) backbone; <sup>b</sup> For HPLC conditions, consult Experimental Procedures; <sup>c</sup> 2'-O-(2-methoxyethyl) ribonucleotide residues are italicized; C stands for 5-methyl-2'-O-(2-methoxyethyl)cytidine residue.

22

Please delete the paragraph spanning page 49 of the specification and replace it with the following new paragraph.

Table 3.ESMS data oligonucleotides 33-40.<sup>a</sup>

	Sequence, 5' to 3'	Backbone	ESMS, found	Molecular Formula	ESMS, calculated
33	DMTr-TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpO <SEQ. ID. NO. 4>	P=O	6365.2	C <sub>211</sub> H <sub>263</sub> N <sub>71</sub> O <sub>122</sub> P <sub>20</sub>	6365.2
34	DMTr-TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpS <SEQ. ID. NO. 5>	P=O	6381.7	C <sub>211</sub> H <sub>263</sub> N <sub>71</sub> O <sub>121</sub> P <sub>20</sub> S	6381.3
35	DMTr-TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpS <SEQ. ID. NO. 5>	P=S	6686.9	C <sub>211</sub> H <sub>263</sub> N <sub>71</sub> O <sub>102</sub> P <sub>20</sub> S <sub>20</sub>	6686.5
36	TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpO <SEQ. ID. NO. 6>	P=O	6062.2	C <sub>190</sub> H <sub>245</sub> N <sub>71</sub> O <sub>120</sub> P <sub>20</sub>	6062.8
37	TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpS <SEQ. ID. NO. 7>	P=O	6079.4	C <sub>190</sub> H <sub>245</sub> N <sub>71</sub> O <sub>119</sub> P <sub>20</sub> S	6078.9
38	TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpS <SEQ. ID. NO. 7>	P=S	6384.7	C <sub>190</sub> H <sub>245</sub> N <sub>71</sub> O <sub>100</sub> P <sub>20</sub> S <sub>20</sub>	6384.2
39	TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpS-Pyr <SEQ. ID. NO. 8>	P=O	6350.9	C <sub>209</sub> H <sub>258</sub> N <sub>72</sub> O <sub>120</sub> P <sub>20</sub> S	6350.2
40	TGCATC <sub>5</sub> AG <sub>2</sub> C <sub>2</sub> AC <sub>2</sub> ATpS-Flu <SEQ. ID. NO. 9>	P=O	6467.0	C <sub>212</sub> H <sub>258</sub> N <sub>72</sub> O <sub>125</sub> P <sub>20</sub> S	6466.2

Please delete the paragraph spanning page 77 of the specification and replace it with the following new paragraph.

Table 9: Cholesterol-Conjugated Oligonucleotides (4)

Cmpd	Sequence (5' – 3')	Backbone	Quantity	MW		More Info
				calc	Found	
A3						